

## SEQUENCE PROTOCOL

&lt;110&gt; Degussa AG

5 &lt;120&gt; Nucleotide sequences which code for the dep67 gene

&lt;130&gt; 000565 BT

10 &lt;140&gt;

&lt;141&gt;

&lt;160&gt; 4

15 &lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1786

&lt;212&gt; DNA

20 &lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (259)..(1560)

25 &lt;223&gt; dep67 gene

&lt;400&gt; 1

cgccgcgttttc cgagcgggttgc tctagcgc当地 cgagtgc当地 accgc当地 ttgtt tgccctggc 60

30 tggcgc当地 gtgttttgcc acgtgc当地 cattgc当地 gctc ggacttaaaa ttcaac当地 cc当地 120

cagatgg当地 tc当地 aaggc当地 ctgt gaaatgaggc staggc当地 cgc gacgc当地 ttcc agagaaa当地 180

caggcataac cc当地 taaaata cc当地 ctgtatcc ttcc cggc当地 ctgccccctg gtccccc当地 240

35 gc当地 tacataa taggacgc atg gga aaa cat gag gtt gct cag cag acg gtt 291

Met	Gly	His	Glu	Val	Ala	Gln	Gln	Thr	Val
1			5					10	

40 cc当地 ggt cct tc当地 cc当地 gaa atg gaa gcg cag cc当地 cgt aaa gag tt当地 cgc 339  
 Pro Gly Pro Ser Pro Glu Met Glu Ala Gln Arg Arg Lys Glu Leu Arg  
 15 20 2545 aag cac aag gcc att gcc act ggc ctg tt当地 att tt当地 gct gcc gct gta 387  
 Lys His Lys Ala Ile Ala Thr Gly Leu Leu Ile Phe Ala Ala Ala Val  
 30 35 4050 tat tt当地 ttc cgt tt当地 gt当地 gag acc cgt cc当地 ggt gaa act gca gcg 435  
 Tyr Phe Leu Cys Arg Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala  
 45 50 5555 tgg gta ggt tt当地 gt当地 cgc gct gcg gca gag gcc gga atg att ggc ggg 483  
 Trp Val Gly Phe Val Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly  
 60 65 70 7555 tt当地 gcc gac tt当地 gtc acc gcg ctg tt当地 cgt cat cca tt当地 tgg 531  
 Leu Ala Asp Trp Phe Ala Val Thr Ala Leu Phe Arg His Pro Leu Trp  
 80 85 90

	ctg cct att ccg cac act gcg att atc ccg cgc aag aaa gac cag tta Leu Pro Ile Pro His Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu 95	100	105	579
5	ggt gag gcc tta agc ggg ttt gtc ggg gat aac ttc cta aat gcc cag Gly Glu Ala Leu Ser Gly Phe Val Gly Asp Asn Phe Leu Asn Ala Gln 110	115	120	627
10	ctc att acg gaa aaa gtc tct cag ccg cgg atc cca gag cgc gcc ggg Leu Ile Thr Glu Lys Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly 125	130	135	675
15	gag tgg ctc gcc cag ccg gaa aac ggg gag aaa gtt tcg cgc gaa gtc Glu Trp Leu Ala Gln Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val 140	145	150	723
20	ggc aaa ttg acc gct aat att gtc cgc gca atc gat ccg tca gat gct Gly Lys Leu Thr Ala Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala 160	165	170	771
25	gaa gcg gtg att aaa tct gcg gtg atc gac aag ctt gcg gaa ccc acc Glu Ala Val Ile Lys Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr 175	180	185	819
30	tgg ggc cca cca gct ggg ccg ttg ctg gaa caa ctc ctc gcc gaa gca Trp Gly Pro Pro Ala Gly Arg Leu Leu Glu Gln Leu Leu Ala Glu Ala 190	195	200	867
35	aag ccg aac cag ttg tcc agg aac tcg cgc agt ggc tgc aca aaa agg Lys Pro Asn Gln Leu Ser Arg Asn Ser Arg Ser Gly Cys Thr Lys Arg 205	210	215	915
40	cgt tgg gct ccc gag ccg ctg att gat cgc ctg ctc aac gag cgc cgc Arg Trp Ala Pro Glu Pro Leu Ile Asp Arg Leu Leu Asn Glu Arg Arg 220	225	230	963
45	ccg att tgg gcg ccg aaa ttc act gcg cag ctg gtc agc ggc aaa gtc Pro Ile Trp Ala Pro Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val 240	245	250	1011
50	tat gac gag gtc ata aaa ttc act gaa gcc gtc gct gcc gat cct aac Tyr Asp Glu Val Ile Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn 255	260	265	1059
55	cac gag gcc cgc aaa tcg ctg cgc cga ttc ctt aat aaa ttg gcg caa His Glu Ala Arg Lys Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Gln 270	275	280	1107
60	gac ctg cag cat gac cca ggc atg att att aaa gtt gaa gaa atc aaa Asp Leu Gln His Asp Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys 285	290	295	1155
65	cgc gac atc atg ggc tcc ggc gcc atc gcg caa gcc gcg cca acc atc Arg Asp Ile Met Gly Ser Gly Ala Ile Ala Gln Ala Ala Pro Thr Ile 300	305	310	1203
70	tgg gcg tca gcc tcc gag tcg ctc att gaa tcc gca gaa gat gag tca Trp Ala Ser Ala Ser Glu Ser Leu Ile Glu Ser Ala Glu Asp Glu Ser 320	325	330	1251

	tca att ctg cgt cgc aaa att gcc gaa gca gct acc acc tgg ggt caa Ser Ile Leu Arg Arg Lys Ile Ala Glu Ala Ala Thr Ser Trp Gly Gln 335 340 345	1299
5	aga ttg ctt gtc gac gac tcc ctc cggtt cat tca ctc gac acc cggtt att Arg Leu Leu Val Asp Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile 350 355 360	1347
10	acc ggc gcc gct gct ttc ctc gcc gac aat tac gcc ccc gaa gtc acc Thr Gly Ala Ala Ala Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr 365 370 375	1395
15	ggc att atc tcc gaa acc att gaa cga tgg gac gct gaa gaa gct tca Gly Ile Ile Ser Glu Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser 380 385 390 395	1443
20	gag aaa atc gaa ctc atg gtg ggc aaa gac ctc caa tac atc cgc ctt Glu Lys Ile Glu Leu Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu 400 405 410	1491
25	aat ggc aca att gta ggt gca tta gca gga ctg gcc att tac gct att Asn Gly Thr Ile Val Gly Ala Leu Ala Gly Leu Ala Ile Tyr Ala Ile 415 420 425	1539
	tcc cat atc ctc ttc gga gct taactaggag taaccatcat gtccgatgca Ser His Ile Leu Phe Gly Ala 430	1590
30	aaagacgatt ccatcttgc caaagtggagc aatgcagctt ccgagcttag cggtgccgtc 1650 agtggatgtcgaaagaactcgatctgtgaga agggaaacctt cagcaagctt 1710 aaaaccgaaag ccagcgaagc cgtcgatcaa gcaaagtccg gtcctcacct agatgccgt 1770 aagaaattcg cccgcg 1786	
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50	Ala Thr Gly Leu Leu Ile Phe Ala Ala Ala Val Tyr Phe Leu Cys Arg 35 40 45	
55	Phe Val Glu Thr Arg Pro Gly Glu Thr Ala Ala Trp Val Gly Phe Val 50 55 60	
	Arg Ala Ala Ala Glu Ala Gly Met Ile Gly Gly Leu Ala Asp Trp Phe 65 70 75 80	

Ala Val Thr Ala Leu Phe Arg His Pro Leu Trp Leu Pro Ile Pro His  
 85 90 95

5 Thr Ala Ile Ile Pro Arg Lys Lys Asp Gln Leu Gly Glu Ala Leu Ser  
 100 105 110

Gly Phe Val Gly Asp Asn Phe Leu Asn Ala Gln Leu Ile Thr Glu Lys  
 115 120 125

10 Val Ser Gln Ala Arg Ile Pro Glu Arg Ala Gly Glu Trp Leu Ala Gln  
 130 135 140

Pro Glu Asn Gly Glu Lys Val Ser Arg Glu Val Gly Lys Leu Thr Ala  
 145 150 155 160

15 Asn Ile Val Arg Ala Ile Asp Pro Ser Asp Ala Glu Ala Val Ile Lys  
 165 170 175

20 Ser Ala Val Ile Asp Lys Leu Ala Glu Pro Thr Trp Gly Pro Pro Ala  
 180 185 190

Gly Arg Leu Leu Glu Gln Leu Leu Ala Glu Ala Lys Pro Asn Gln Leu  
 195 200 205

25 Ser Arg Asn Ser Arg Ser Gly Cys Thr Lys Arg Arg Trp Ala Pro Glu  
 210 215 220

Pro Leu Ile Asp Arg Leu Leu Asn Glu Arg Arg Pro Ile Trp Ala Pro  
 225 230 235 240

30 Lys Phe Thr Ala Gln Leu Val Ser Gly Lys Val Tyr Asp Glu Val Ile  
 245 250 255

35 Lys Phe Thr Glu Ala Val Ala Ala Asp Pro Asn His Glu Ala Arg Lys  
 260 265 270

Ser Leu Arg Arg Phe Leu Asn Lys Leu Ala Gln Asp Leu Gln His Asp  
 275 280 285

40 Pro Gly Met Ile Ile Lys Val Glu Glu Ile Lys Arg Asp Ile Met Gly  
 290 295 300

Ser Gly Ala Ile Ala Gln Ala Ala Pro Thr Ile Trp Ala Ser Ala Ser  
 305 310 315 320

45 Glu Ser Leu Ile Glu Ser Ala Glu Asp Glu Ser Ser Ile Leu Arg Arg  
 325 330 335

50 Lys Ile Ala Glu Ala Ala Thr Ser Trp Gly Gln Arg Leu Leu Val Asp  
 340 345 350

Asp Ser Leu Arg His Ser Leu Asp Thr Arg Ile Thr Gly Ala Ala Ala  
 355 360 365

55 Phe Leu Ala Asp Asn Tyr Ala Pro Glu Val Thr Gly Ile Ile Ser Glu  
 370 375 380

Thr Ile Glu Arg Trp Asp Ala Glu Glu Ala Ser Glu Lys Ile Glu Leu  
 385 390 395 400

Met Val Gly Lys Asp Leu Gln Tyr Ile Arg Leu Asn Gly Thr Ile Val  
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Gly Ala

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dep67-ex1

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dep67-ex2

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